



1

SEQUENCE LISTING

<110> GORSKI, DAVID H.  
WALSH, KENNETH

<120> GROWTH ARREST HOMEBOX GENE

<130> 22311/04015

<140> 09/940,673

<141> 2001-08-27

<150> 09/078,465

<151> 1998-05-14

<150> 08/203,532

<151> 1994-02-24

<160> 19

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (197)..(1105)

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agtgaaaagt gacagcgctt ggtggacttt gggaccttcg tgaagtcttc tgcttgggaag 180

ctgagacttg catgcc atg gaa cac ccc ctc ttt ggc tgc ctg cgc agc ccc 232

Met Glu His Pro Leu Phe Gly Cys Leu Arg Ser Pro  
1 5 10

cac gcc aca gcg caa ggc ttg cac ccc ttc tcg cag tct tct ctg gcc 280

His Ala Thr Ala Gln Gly Leu His Pro Phe Ser Gln Ser Ser Leu Ala  
15 20 25

ctc cat gga aga tct gac cac atg tcc tac ccc gaa ctc tcc aca tct 328

Leu His Gly Arg Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr Ser  
30 35 40

tcc tcg tct tgc ata atc gcg gga tac ccc aat gag gag ggc atg ttt 376

Ser Ser Ser Cys Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met Phe  
45 50 55 60

gcc agc cag cat cac agg ggg cac cac cac cac cac cac cac cat 424

Ala Ser Gln His His Arg Gly His His His His His His His His  
65 70 75

cac cac cac cag cag cag cag cac cag gct ctg caa agc aac tgg cac	472
His His His Gln Gln Gln Gln His Gln Ala Leu Gln Ser Asn Trp His	
80 85 90	
ctc ccg cag atg tcc tcc ccg cca agc gcg gcc cgg cac agc ctt tgc	520
Leu Pro Gln Met Ser Ser Pro Pro Ser Ala Ala Arg His Ser Leu Cys	
95 100 105	
ctg cag cct gat tcc gga ggg ccc ccg gag ctg ggg agc agc cct ccg	568
Leu Gln Pro Asp Ser Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro Pro	
110 115 120	
gtc ctg tgc tcc aac tct tct agc ctg ggc tcc agc acc ccg acc gga	616
Val Leu Cys Ser Asn Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr Gly	
125 130 135 140	
gcc gcg tgc gca cca agg gat tat ggc cgt caa gcg ctg tca ccc gca	664
Ala Ala Cys Ala Pro Arg Asp Tyr Gly Arg Gln Ala Leu Ser Pro Ala	
145 150 155	
gaa gtg gag aag aga agt ggc agc aaa aga aaa agc gac agt tca gat	712
Glu Val Glu Lys Arg Ser Gly Ser Lys Arg Lys Ser Asp Ser Ser Asp	
160 165 170	
tcc cag gaa gga aat tac aag tca gaa gtg aac agc aaa cct agg aag	760
Ser Gln Glu Gly Asn Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg Lys	
175 180 185	
gaa aga aca gct ttc acc aaa gag caa atc aga gaa ctt gag gca gag	808
Glu Arg Thr Ala Phe Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala Glu	
190 195 200	
ttc gcc cat cat aac tat ctg acc aga ctg aga aga tat gag ata gcg	856
Phe Ala His His Asn Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile Ala	
205 210 215 220	
gtg aac cta gac ctc act gaa aga cag gtg aaa gtg tgg ttc cag aac	904
Val Asn Leu Asp Leu Thr Glu Arg Gln Val Lys Val Trp Phe Gln Asn	
225 230 235	
agg aga atg aag tgg aag ccg gtc aag ggg gga caa caa gga gct gca	952
Arg Arg Met Lys Trp Lys Arg Val Lys Gly Gly Gln Gln Gly Ala Ala	
240 245 250	
gcc cga gaa aag gaa ctg gtg aat gtg aaa aag gga aca ctt ctt cca	1000
Ala Arg Glu Lys Glu Leu Val Asn Val Lys Lys Gly Thr Leu Leu Pro	
255 260 265	
tca gag ctg tca gga att ggt gca gcc acc ctc cag cag aca ggg gac	1048
Ser Glu Leu Ser Gly Ile Gly Ala Ala Thr Leu Gln Gln Thr Gly Asp	
270 275 280	
tca cta gca aat gac gac agt cgc gat agt gac cac agc tct gag cac	1096
Ser Leu Ala Asn Asp Asp Ser Arg Asp Ser Asp His Ser Ser Glu His	
285 290 295 300	
gca cac tta tgatacatag agagaccagc tccgtttctca ggaaagcacc	1145
Ala His Leu	

attgtgatgg caaatctcac ccaaacatcg ttacatggc agatgactgt ggcagtgttg 1205  
 cttaatataa ttaaacgcag gcatctcaag tctgtttctc atgattgata gaagggtttac 1265  
 actaagtgcc tcttattgaa gatgcttcca cagtgaatt ggagaaagtg aacatatcta 1325  
 aatatacttg ttccttatat gacagagagg gagatgaatg tttgctttgg cttgcaactga 1385  
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 caaagctagt tcttcaaggg atagatgaga aactgaatgt ctgacaagta gactcagcga 2165  
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 <213> Rattus sp.

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 Gln Gly Leu His Pro Phe Ser Gln Ser Leu Ala Leu His Gly Arg  
 20 25 30  
 Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr Ser Ser Ser Ser Cys  
 35 40 45  
 Ile Ile Ala Gly Tyr Pro Asn Glu Glu Gly Met Phe Ala Ser Gln His  
 50 55 60

His	Arg	Gly	His	His	His	His	His	His	His	His	His	His	His	His	Gln	65	70	75	80
Gln	Gln	Gln	His	Gln	Ala	Leu	Gln	Ser	Asn	Trp	His	Leu	Pro	Gln	Met	85	90	95	
Ser	Ser	Pro	Pro	Ser	Ala	Ala	Arg	His	Ser	Leu	Cys	Leu	Gln	Pro	Asp	100	105	110	
Ser	Gly	Gly	Pro	Pro	Glu	Leu	Gly	Ser	Ser	Pro	Pro	Val	Leu	Cys	Ser	115	120	125	
Asn	Ser	Ser	Ser	Leu	Gly	Ser	Ser	Thr	Pro	Thr	Gly	Ala	Ala	Cys	Ala	130	135	140	
Pro	Arg	Asp	Tyr	Gly	Arg	Gln	Ala	Leu	Ser	Pro	Ala	Glu	Val	Glu	Lys	145	150	155	160
Arg	Ser	Gly	Ser	Lys	Arg	Lys	Ser	Asp	Ser	Ser	Asp	Ser	Gln	Glu	Gly	165	170	175	
Asn	Tyr	Lys	Ser	Glu	Val	Asn	Ser	Lys	Pro	Arg	Lys	Glu	Arg	Thr	Ala	180	185	190	
Phe	Thr	Lys	Glu	Gln	Ile	Arg	Glu	Leu	Glu	Ala	Glu	Phe	Ala	His	His	195	200	205	
Asn	Tyr	Leu	Thr	Arg	Leu	Arg	Arg	Tyr	Glu	Ile	Ala	Val	Asn	Leu	Asp	210	215	220	
Leu	Thr	Glu	Arg	Gln	Val	Lys	Val	Trp	Phe	Gln	Asn	Arg	Arg	Met	Lys	225	230	235	240
Trp	Lys	Arg	Val	Lys	Gly	Gly	Gln	Gln	Gly	Ala	Ala	Ala	Arg	Glu	Lys	245	250	255	
Glu	Leu	Val	Asn	Val	Lys	Lys	Gly	Thr	Leu	Leu	Pro	Ser	Glu	Leu	Ser	260	265	270	
Gly	Ile	Gly	Ala	Ala	Thr	Leu	Gln	Gln	Thr	Gly	Asp	Ser	Leu	Ala	Asn	275	280	285	
Asp	Asp	Ser	Arg	Asp	Ser	Asp	His	Ser	Ser	Glu	His	Ala	His	Leu		290	295	300	

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	1				5											
tgc	ctg	cgc	agc	cct	cac	gcc	acg	gcg	caa	ggc	ttg	cac	ccg	ttc	tcc	101
Cys	Leu	Arg	Ser	Pro	His	Ala	Thr	Ala	Gln	Gly	Leu	His	Pro	Phe	Ser	
	10					15					20					
caa	tcc	tct	ctc	gcc	ctc	cat	gga	aga	tct	gac	cat	atg	tct	tac	ccc	149
Gln	Ser	Ser	Leu	Ala	Leu	His	Gly	Arg	Ser	Asp	His	Met	Ser	Tyr	Pro	
	25					30					35					
gag	ctc	tct	act	tct	tcc	tca	tct	tgc	ata	atc	gcg	gga	tac	ccc	aac	197
Glu	Leu	Ser	Thr	Ser	Ser	Ser	Ser	Cys	Ile	Ile	Ala	Gly	Tyr	Pro	Asn	
	40				45				50						55	
gaa	gag	gac	atg	ttt	gcc	agc	cag	cat	cac	agg	ggg	cac	cac	cac	cac	245
Glu	Glu	Asp	Met	Phe	Ala	Ser	Gln	His	His	Arg	Gly	His	His	His	His	
				60					65					70		
cac	cac	cac	cat	cac	cac	cat	cag	cag	cag	cag	cac	cag	gct	ctg	caa	293
His	His	His	His	His	His	His	Gln	Gln	Gln	Gln	His	Gln	Ala	Leu	Gln	
			75				80						85			
acc	aac	tgg	cac	ctc	ccg	cag	atg	tct	tcc	cca	ccg	agt	gcg	gct	cgg	341
Thr	Asn	Trp	His	Leu	Pro	Gln	Met	Ser	Ser	Pro	Pro	Ser	Ala	Ala	Arg	
	90					95						100				
cat	agc	ctc	tgc	ctc	cag	ccc	gac	tct	gga	ggg	ccc	cca	gag	ttg	ggg	389
His	Ser	Leu	Cys	Leu	Gln	Pro	Asp	Ser	Gly	Gly	Pro	Pro	Glu	Leu	Gly	
	105				110						115					
agc	agc	ccg	ccc	gtc	ctg	tgc	tcc	aac	tct	tcc	agc	ttg	ggc	tcc	agc	437
Ser	Ser	Pro	Pro	Val	Leu	Cys	Ser	Asn	Ser	Ser	Ser	Leu	Gly	Ser	Ser	
	120				125				130					135		
acc	ccg	act	ggg	gcc	gcg	tgc	gcg	ccg	ggg	gac	tac	ggc	cgc	cag	gca	485
Thr	Pro	Thr	Gly	Ala	Ala	Cys	Ala	Pro	Gly	Asp	Tyr	Gly	Arg	Gln	Ala	
			140					145						150		
ctg	tca	cct	gcg	gag	gcg	gag	aag	cga	agc	ggc	ggc	aag	agg	aaa	agc	533
Leu	Ser	Pro	Ala	Glu	Ala	Glu	Lys	Arg	Ser	Gly	Gly	Lys	Arg	Lys	Ser	
		155					160						165			
gac	agc	tca	gac	tcc	cag	gaa	gga	aat	tac	aag	tca	gaa	gtc	aac	agc	581
Asp	Ser	Ser	Asp	Ser	Gln	Glu	Gly	Asn	Tyr	Lys	Ser	Glu	Val	Asn	Ser	
	170					175						180				
aaa	ccc	agg	aaa	gaa	agg	aca	gca	ttt	acc	aaa	gag	caa	atc	aga	gaa	629
Lys	Pro	Arg	Lys	Glu	Arg	Thr	Ala	Phe	Thr	Lys	Glu	Gln	Ile	Arg	Glu	
	185					190				195						
ctt	gaa	gca	gaa	ttt	gcc	cat	cat	aat	tat	ctc	acc	aga	ctg	agg	cga	677
Leu	Glu	Ala	Glu	Phe	Ala	His	His	Asn	Tyr	Leu	Thr	Arg	Leu	Arg	Arg	
	200				205					210					215	

tac gag ata gca gtg aat ctg gat ctc act gaa aga cag gta aaa gtc 725  
 Tyr Glu Ile Ala Val Asn Leu Asp Leu Thr Glu Arg Gln Val Lys Val  
                                   220                                  225                                  230

tgg ttc caa aac agg cgg atg aag tgg aag agg gta aag ggt gga cag 773  
 Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Arg Val Lys Gly Gly Gln  
                                   235                                  240                                  245

caa gga gct gcg gct cgg gaa aag gaa ctg gtg aat gtg aaa aag gga 821  
 Gln Gly Ala Ala Ala Arg Glu Lys Glu Leu Val Asn Val Lys Lys Gly  
                                   250                                  255                                  260

aca ctt ctc cca tca gag ctg tcg gga att ggt gca gcc acc ctc cag 869  
 Thr Leu Leu Pro Ser Glu Leu Ser Gly Ile Gly Ala Ala Thr Leu Gln  
                                   265                                  270                                  275

caa aca ggg gac tct ata gca aat gaa gac agt cac gac agt gac cac 917  
 Gln Thr Gly Asp Ser Ile Ala Asn Glu Asp Ser His Asp Ser Asp His  
 280                                  285                                  290                                  295

agc tca gag cac gcc cac ctc tga 941  
 Ser Ser Glu His Ala His Leu  
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<211> 302

<212> PRT

<213> Homo sapiens

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                                   20                                  25                                  30

Ser Asp His Met Ser Tyr Pro Glu Leu Ser Thr Ser Ser Ser Cys  
                                   35                                  40                                  45

Ile Ile Ala Gly Tyr Pro Asn Glu Glu Asp Met Phe Ala Ser Gln His  
   50                                  55                                  60

His Arg Gly His His His His His His His His His His His Gln Gln  
   65                                  70                                  75                                  80

Gln Gln His Gln Ala Leu Gln Thr Asn Trp His Leu Pro Gln Met Ser  
                                   85                                  90                                  95

Ser Pro Pro Ser Ala Ala Arg His Ser Leu Cys Leu Gln Pro Asp Ser  
                                   100                                  105                                  110

Gly Gly Pro Pro Glu Leu Gly Ser Ser Pro Pro Val Leu Cys Ser Asn  
                                   115                                  120                                  125

Ser Ser Ser Leu Gly Ser Ser Thr Pro Thr Gly Ala Ala Cys Ala Pro  
   130                                  135                                  140

Gly Asp Tyr Gly Arg Gln Ala Leu Ser Pro Ala Glu Ala Glu Lys Arg  
 145 150 155 160  
 Ser Gly Gly Lys Arg Lys Ser Asp Ser Ser Asp Ser Gln Glu Gly Asn  
 165 170 175  
 Tyr Lys Ser Glu Val Asn Ser Lys Pro Arg Lys Glu Arg Thr Ala Phe  
 180 185 190  
 Thr Lys Glu Gln Ile Arg Glu Leu Glu Ala Glu Phe Ala His His Asn  
 195 200 205  
 Tyr Leu Thr Arg Leu Arg Arg Tyr Glu Ile Ala Val Asn Leu Asp Leu  
 210 215 220  
 Thr Glu Arg Gln Val Lys Val Trp Phe Gln Asn Arg Arg Met Lys Trp  
 225 230 235 240  
 Lys Arg Val Lys Gly Gly Gln Gln Gly Ala Ala Ala Arg Glu Lys Glu  
 245 250 255  
 Leu Val Asn Val Lys Lys Gly Thr Leu Leu Pro Ser Glu Leu Ser Gly  
 260 265 270  
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 275 280 285  
 Asp Ser His Asp Ser Asp His Ser Ser Glu His Ala His Leu  
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 29-mer oligonucleotide

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 <222> (6)  
 <223> inosine

<220>  
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 <222> (21)  
 <223> inosine

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<400> 5  
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<210> 6  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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 <222> (10)  
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<400> 6  
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18

<210> 7  
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 <212> DNA  
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<210> 9  
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<210> 19

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<212> DNA

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<223> Description of Artificial Sequence: Synthetic  
Primer

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